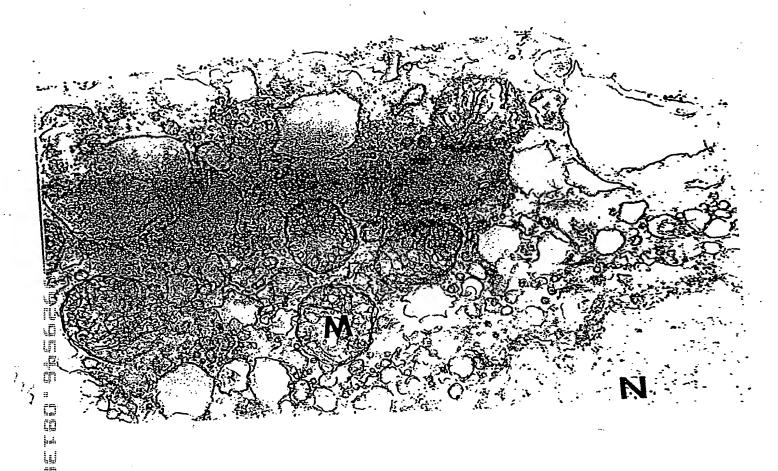


PRESS MAIL <u>EL360933802US</u> ATTY. DKT. 266/186 SHEET 1 OF 12







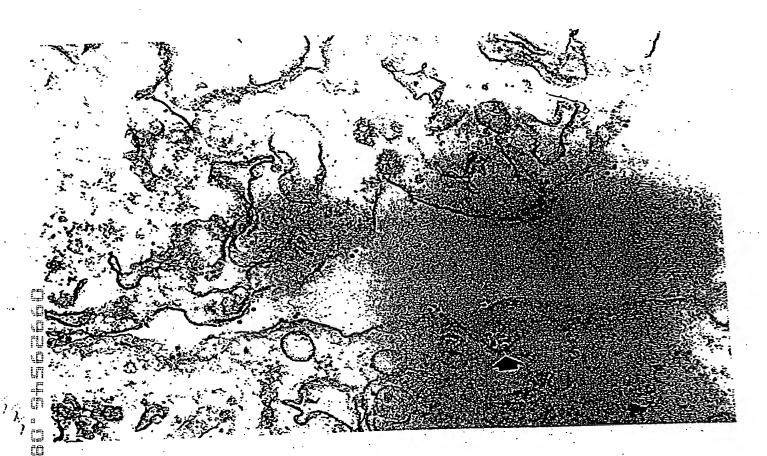


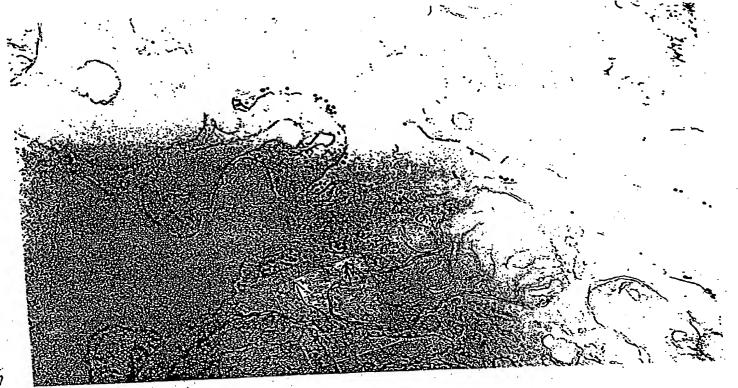
FIGURE 2





E...RESS MAIL <u>EL360933802US</u> ATTY. DKT. 266/186 SHEET 4 OF 12





EL369933802US ATTY. DKT. 266/186 SHEET 5 OF 12



EX. RESS MAIL <u>EL360933802US</u> ATTY. DKT. 266/186 SHEET 6 OF 12

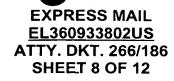
VH1E.SEQ(1>267)
VH3E.SEQ(1>264)
VH4E.SEQ(1>210)
VH1E.SEQ(1>115)
VH12UE.SEQ(1>137)
VH15UE.SEQ(1>130)
VH1FORE.SEQ(1>207)
VH3FORE.SEQ(1>207)
VH4FORE.SEQ(1>230)
VH3E.SEQ(1>131)
VH12E.SEQ(1>131)
VH1UE.SEQ(1>109)
VH1UE.SEQ(1>42)



## EXPRESS MAIL 360933802US ATY. DKT. 266/186 SHEET 7 OF 12

Enzymes: All 74 enzymes (No Filter).  Settings: Linear, Certain Sites Only, Standard Genetic Code  Linear, Certain Sites Only, Standard Genetic Code  Enzymes : Fro57 I
Due! Avail 100011
Sauge   Paul Sauge   Sauge
SEQ. ID. NO. 1 TCTCCTGTCAGGAACTGCAGGTGTCCTCTCTGAGGTCCAGCTGCAACAGTCTGGACCTGGACCTGAACTGGTGAACTGCAGGTGAACTGCAGGTGAACTGCAACTTC
L
SEA TO NO. 3 SPYRNCKCY SEVOLOGS CHELLY S
SEQ. ID. NO. 4 L S C O E L O V S S L R S S C N S L D L N W . 3
SEQ. ID. NO. 5 pratti
Bsr (
Hph I ExpR V III
11. TECTOCA AGACTTCTGGATACACATICACIGACIATICACIATICATIC
SEQ. ID. NO. 1 CCTGGGACTTCAGTGAGGACTATCTGAAGACCTATGTGTAAGTGACTTATATGGTATGTGACCC SEQ. ID. NO. 2 GGACCCTGAAGTCACTCCTATAGGACGTTCTGAAGACCTATGTGTAAGTGACTTATATGGTATGTGACCC
SEQ. ID. NO. 2 GGACCCTGAAGTCACTCCTATAGGACTCATAGGACTACATAGGACTCATAGGACTCATAGGACTCATAGGACTCATAGGACTCATAGGACTCATAGGACTACATAGGACTCATAGGACTCATAGGACTCATAGGACTCATAGGACTCATAGGACTCATAGGACTACATAGGACTCATAGGACTCATAGGACTCATAGGACTAGACT
and a second to the second sec
DERCE TO A P. G. T. S. V. R. L. D. T. H. S. L. R. T. L. T. L. R. T
DEM ID: NO
SEQ. ID. NO. 5
HDQ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
NOT 1 TGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGAAACATCCTAACAATGGTGGTACCACCTA 210
SEQ. ID. NO. 1 TGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGGTTAGCTAGC
SEQ. ID. NO. 2 ACTTCGTCTCGGTACCTTTCTCGGAACTCACCTAACCTTACCTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTACCTACCTTACCTACCTTACCTACCTACCTTACCTAC
DEQ. 120 TY
SEQ. ID. NO. 3 Y K Q S H G K 3 C C L E T S I C V V
SEQ. ID. NO. 4 . S R A H E R A C
/ SEQ. ID. NO. 5
, Berl Rsal   Sact
Tag1 Hae III Acc1 Bsr1 Rsa1
280
SEQ. ID. TO
SEQ. ID. NO.
SDQ. ID. NO NO. K. F. C.
SEO. ID. NO. 4 T T R S S N
SEQ. ID. NO. 5
Alu     Hae III
Dde I. Hinf! PSt! [1]
Dde 1. Hinf PST   Dde 1. Hinf
DING
SEQ. ID. NO. 2 GCGTCGGATTGTAGACTCCTAAGACTACTAAGACTCCTAAGACTACAACTCCTAAGACTCCTAAGACTA
GECSC CAAGWNED TWG
SEQ. ID. NO. 3 POPNISEDS AV-YYCAAGWNFLTTEA
SEQ. ID. NO. 5
A1061
pde t
SEO TO NO. 1 AAGGCACCACTCTCACAGTCTCCTCAGCCAAAACGACACCC 391
SEQ. ID. NO. 1 AAGGCACCACITICACAGGAGTGGGTTTTGCTGTGGG
CEO THE NO. 2 TICCGTGGTGAGAGIGTCAGAGGAGG
SONOT
SEO. TD. NO. 3 R H H S H S L S A K T T P
SEQ. ID. NO. K A P L 3 O S
SEQ. ID. NO. 5

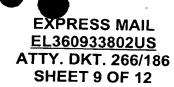
ζ



Lipman-Pearson Prote Ktuple: 2; Gap Penalt Seq1(1>115) J591VH:PRO	Seq2(1>125) MUVHIIA.PRO	Penalty: 12 Similarity Index 75.6	Gap Number 2	Gap Co Length	Dinsensus Length 125	
(1>115)  EVOLOOSGPELVKPGT EVOLOOSGPELVKPGT EVOLOOSGPELVKPGT	CSVRISCKTSGYTF	€30 TEYTI-HWYKO	SHGKSLEWIG IS GKSLEWIG ISPGKSLEWIG 40	50 - 6	60	
-60 YNOKFEDKATLTYDK	F80 SSTAYMELRSLTS	. <b>√8</b> 0 ≈EDSAVYÝCAA	G	INFDYWGOGTT FDYWGOGTT YAFDYWGOGTT	120	. * 

3

LTVSS :T:VSS VTVSS



VK15E.SEQ(1>124)
VK16E.SEQ(1>116)
VK20E.SEQ(1>153)
VK27UE.SEQ(1>153)
VK28UE.SEQ(1>153)
VK18E.SEQ(1>153)
VK26UE.SEQ(1>153)
VK26UE.SEQ(1>153)
VK26UE.SEQ(1>153)
VK25UE.SEQ(1>263)
VK25UE.SEQ(1>263)
VK25UE.SEQ(1>209)
VK16UE.SEQ(1>1442)
VK18UE.SEQ(1>180)



EXPRESS MAIL 1360933802US ATTY. DKT. 266/186 SHEET 10 OF 12

All 74 enzymes (No Filler) Linear, Certain Siles Only, Standard Genetic Code Hph I Enzymes: Settings: TTATATGGAGCTGATGGGAACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCAGTAGGAGAGA SEQ. ID. NO. 10 AATATACCTCGACTACCCTTGTAACATTACTGGGTTAGGGGGTTAGGTACAGGTACAGGTCATCCTCTCT T V H T Q S P K S H S H T L P N L P N P C P C Q . E T L P N L P N P C P C Q . E H C N O P I S Q I H V H V S R Y H E L H G r A C SEQ. ID. NO. 11 SEQ. ID. NO. 12 ε SEQ. ID. NO. 13 GGGTCACCTIGACCTGCAAGGCCAGTGAGAATGTGGTTACTTATGTTTCCTGGTATCAACAGAAACCAGA Bsrl SEQ. ID. NO. 10 CCCAGTGGAACTGGACGTTCCGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTTGGTCT SEQ. ID. NO. 9 R V T L T C K A S E N V V T Y V S Y Y Q Q K P E G S P P A R P V R H V L L H F P G T N R N Q C G H L D L Q G Q . E. C G Y L C F L V S T E T R SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13 Ava II Dpn I Bsa0 I Sau96 I Pvu I Rsa1 GCAGTCTCCTAAACTGCTGATATACGGGGCATCCAACCGGTACACTGGGGTCCCCGATCGCTTCACAGGC SEQ. ID. NO. 10 CGTCAGAGGATTTGACGACTATATGCCCCGTAGGTTGGCCATGTGACCCCAGGGGCTAGCGAAGTGTCCG SEQ. ID. NO. 9 QSPKLLIYGASHRYT SLLNC YTGHP-TGT AVS.TADIRGIQPYH P·I T L SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13 Mbo II E0057 I Bsp6 II Mbo1 Opn i AGTGGATCTGCAACAGATTTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTATCACT TEACCTAGACGTTGTCTAAAGTGAGACTGGTAGTCGTCACACGTCCGACTTCTGGAACGTCTAATAGTGA SEQ. ID. NO. 9. S G S A T O F T L T I S S V Q A E D L A D Y
V D. L Q Q I S L P S A V. C R L K T L Q I
Q W I C N R F H S O H Q Q C A G . R P C R L · SEQ. · ID. · NO. 10 SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13 Ava II · Sau961 Alui Rsa I GTGGACAGGGTTACAGCTATCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGC 350 CACCTGTCCCAATGTCGATAGGCATGTGCAAGCCTCCCCCCTGGTTCGACCTTTATTTTGCCCGACTACG SEQ. ID. NO. 9 Y P Y T F G G G T K L E I K R . R T R S E G G P S W K . N . S V H V R R G D Q A G N K T SEQ. ID. NO. 10 V D R V T A SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13 TGCACCAACTGTA 363. SEQ. ID. NO. 9 ACGTGGTTGACAT SEQ. ID. NO. 10 A P. T. V SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13

	in Alignment y: 4; Gap Length Seq2(1>111) MUVKV.PRO	Penalty: 12 Similarity Index	Gap Number	Gap Length	Conse Le	nsus ngth
J591VK.PRO (1>107)	(1>109)	60.4	2 .	2	·.	109
#10 NIVMTOSPKSMSMSVG : I MTOSP.S:S S:G DIOMTOSPSSLSASLG 40 #60 DREIGSGSATOFILTI .RE:GSGS:TD::LT. SRESGSGSGTDYSLT	RVT:TC:AS :: DRVTITCRASODD 420 480 ESSVOAEDLADYHO	VVTYVSWYOOK : Y: WYOOK ISNYLNWYOOK -30 -90 GOGYSY-PYTF	PEOSPKLLIYG P. SPKLLIY PGGSPKLLIYY 40 4! √100: GGGTKLEIK GGGTKLEIK	50 ASNRYTGV AS: :GV (ASRLHSGV	16	

